

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 14, 2001, 16:12:19 ; Search time 21.02 Seconds  
(without alignments)  
1466.551 Million cell updates/sec

Title: US-09-455-486-6  
Perfect score: 2351  
Sequence: 1 MESISMGPXSLSETLPN.....ALVLPISVILLQLICRYPD 454  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues  
Total number of hits satisfying chosen parameters: 195891  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_66:4  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156.5	6.7	239	2 T50571	probable oxidoreductase
2	147	6.3	213	2 H69400	conserved hypothetical
3	142	6.0	212	2 D69361	conserved hypothetical
4	142	6.0	224	2 T10120	F420-dependent NAD
5	133	5.7	223	2 D64487	hypothetical prote
6	120.5	5.1	232	2 A69131	conserved hypothetical
7	119.5	5.1	216	2 T00121	hypothetical prote
8	116.5	5.0	242	2 G82642	conserved hypothetical
9	111.5	4.7	695	1 JN0898	foliitropin recept
10	111.5	4.7	1228	2 S59681	probable membrane
11	110.5	4.7	694	2 JC4301	foliitropin recept
12	109	4.6	320	2 T28379	ORF MSV218 hypothe
13	109	4.6	712	2 S50959	probable membrane
14	109	4.6	1184	2 H71436	hypothetical prote
15	107.5	4.6	629	2 S60385	probable membrane
16	107.5	4.6	695	1 ORRHUT	foliitropin recept
17	105	4.5	442	2 B64582	sodium- and chlori
18	105	4.5	604	2 T31042	hypothetical prote
19	104	4.4	396	1 C64907	chloramphenicol re
20	103	4.4	465	2 S69915	sodium-phosphate t
21	102.5	4.4	1242	2 T39453	probable mra stab
22	102	4.3	574	2 T41068	hypothetical prote
23	101	4.3	320	2 E71139	hypothetical prote
24	101	4.3	348	2 T12284	NADH dehydrogenase
25	101	4.3	420	2 F69144	O-antigen transpor
26	101	4.3	501	2 T02134	hypothetical prote
27	101	4.3	735	2 A83006	hypothetical prote
28	100.5	4.3	346	2 T11181	NADH dehydrogenase
29	100	4.3	395	2 C71219	hypothetical prote

30	100	4.3	476	2 A28439	endonuclease SccI
31	99.5	4.2	452	2 C71391	NADH dehydrogenase
32	98	4.2	348	2 T12290	NADH dehydrogenase
33	98	4.2	348	2 T12281	NADH dehydrogenase
34	98	4.2	442	2 C71930	probable transport
35	98	4.2	962	2 T05845	hypothetical prote
36	98	4.2	3411	1 GNVVY	genome polyprotein
37	98	4.2	3411	1 GNVVYP	genome polyprotein
38	97.5	4.1	268	2 A70417	hypothetical prote
39	97.5	4.1	695	2 I45896	follicle stimulat1
40	97	4.1	345	2 T11325	NADH dehydrogenase
41	97	4.1	348	2 T12283	NADH dehydrogenase
42	97	4.1	692	2 A34548	foliitropin recept
43	96.5	4.1	608	2 G02640	polycystic kidney
44	96.5	4.1	686	2 S30075	ferric reductase (
45	96.5	4.1	711	2 T25281	hypothetical prote

ALIGNMENTS

RESULT 1  
T50571  
Probable oxidoreductase [imported] - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 28-Jul-2000  
C:Accession: T50571  
R:Redenbach, M.; Kieser, H.M.; Denapalte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; H  
Mol. Microbiol. 21, 77-96, 1996  
A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 M.  
A:Reference number: Z20556; MUID:97000351  
A:Accession: T50571  
A:Status: preliminary; Translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-239 <RED>  
A:Cross-references: EMBL:AL133220; PIDN:CAB61708.1  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Note: SCC75A.08c  
C:Superfamily: conserved hypothetical protein MJ1501

Query Match	6.7%	Score 156.5;	DB 2;	Length 239;
Best Local Similarity	27.9%	Pred. No. 3.5e-05;		
Matches	61;	Conservative	41;	Mismatches 72;
			Indels	45;
			Gaps	10;
Qy	25	IKDARKVTGVVI-GSGDFAKSLITRLRCGYHVYIGSR---	NPXFASEFFHVVDVTHHE	80
Db	23	LPDVSGLVVGVGGTGGPOGKGLAYLAKAGOKVIVGSR	AAAAAEEIGHGVGADNA	82
Qy	81	DALAKTNIIFVAIIRE-HYTSIMDLRHLVGLKILIDVSNMIRNO-----	YPE--SNAE	131
Db	83	ETARSDDVIVAVPMDGCHGKTLESRLAEISGLVVDVCPGLGFKKAYALKPEGSAAE		142
Qy	132	YLASFDPDLIVKGVNVYSAWALQ-----	LGPKDASQVYICSNIIQARQOV	178
Db	143	QAALLPDSRVAAAFHLSAVLQDPDEIDTDVWVLGEERADVEI-----	VQA-----	192
Qy	179	TELARQLNFIP-----IDGLSSLSAREIENLPLRLTLWR	213	
Db	193	--LAGR---IPCMRGVFAGRLRNAHQVESLVANLISVNR	226	

RESULT 2  
H69400  
conserved hypothetical protein AF1209 - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 29-Sep-1999  
C:Accession: H69400  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod  
.; Fieischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997

A;Authors: Kaine, B.P.; Borodovsky, M.; Kienk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, J.R.  
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A;Reference number: A64300; MOID:96397959  
A;Accession: D64487  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-223 <BUL>  
A;Cross-references: GB:U67591; GB:L77117; NID:g826422; PIDN:AAB99514.1: PID:g1500389  
C;Genetics:  
C;Map position: REV1473617-1472946  
C;Superfamily: conserved hypothetical protein MJ1501

Query Match            5.7%; Score 133; DB 2: Length 223;  
Best Local Similarity   21.9%; Pred. No. 0.0024;  
Matches   46; Conservative   52; Mismatches   78; Indels   34; Gaps   7;

QY   37   GSDFAKSLTILRLRCYGHVVGISGNPKFASPPHVVDV-----THEDALT   84





Qy 237 HPYARNOQSDFYKPIPIEIVN-----KILP-----IVAITLSL 269  
 Db 534 APYKFSQSKDFKVPESIQLRVFTVQIDWSTLPRFCELPMDLRESFTDEFASLSS 593  
 Qy 270 VYL-----AGLAAAYQLVYGTK-----YRRFP-----PWLETWLOCRK 303  
 Db 594 LYSEVELRTTCHALKVLAENSVSAEBSHHNVLLORFPISEAKKIEYLST-----K 648  
 Qy 304 QLGSLSPFFAMVHVAISLCLPMRRS-----ERYL-----FLMAYQQVHANISWNE 351  
 Db 649 STNLLAVLFNV---YTQTTNARSYLETIDQVLKITSKEDLEKTFNNVCGLLKNSNE 704  
 Qy 352 BEVWRIEYISFGIMSLGLLSL--AVTISIPSVSNALNWRFSFTQSTLGVVALLISTFH 409  
 Db 705 ESSGNVNRKKKPOLATFLLDIIICMITLPSVSSYALFSMF-----LTVNSAD 754  
 Qy 410 VLIYGNKRAFEERYEYV 428  
 Db 755 ALIQ--KRA-----YRIIT 766  
 RESULT 11  
 JC4301  
 N:follicotropin receptor - pig  
 N:Alternate names: follicle-stimulating hormone receptor  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 21-Jan-2000  
 C:Accession: JC4301  
 R:Remy, J.J.; Lahbib-Mansais, Y.; Yerle, M.; Bozon, V.; Couture, L.; Pajot, E.; Grebert, Gene 163, 257-261, 1995  
 A:Title: The porcine follitropin receptor: cDNA cloning, functional expression and chromatinogenesis in male and oogenesis in female.  
 A:Reference number: JC4301; MUID:96011644  
 A:Accession: JC4301  
 A:Molecule type: mRNA  
 A:Residues: 1-694 <RGM>  
 A:Cross-references: GB:L31966  
 A:Experimental source: ovarian granulosa cells  
 A:Comment: This receptor belongs to the family of the G-protein coupled receptors. It has been implicated in male and oogenesis in female.  
 C:Genetics:  
 A:Gene: fshr  
 A:Map position: 3 q2.2-q2.3  
 C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
 C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein  
 F:1-365/Domain: follicle-stimulating hormone binding #status predicted <HOB>  
 F:70-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
 F:366-388/Domain: transmembrane #status predicted <TM1>  
 F:398-420/Domain: transmembrane #status predicted <TM2>  
 F:443-464/Domain: transmembrane #status predicted <TM3>  
 F:485-507/Domain: transmembrane #status predicted <TM4>  
 F:528-549/Domain: transmembrane #status predicted <TM5>  
 F:573-596/Domain: transmembrane #status predicted <TM6>  
 F:608-629/Domain: transmembrane #status predicted <TM7>  
 Query Match 4.7%; Score 110.5; DB 2; Length 694;  
 Best Local Similarity 16.5%; Pred. No. 0.6;  
 Matches 91; Conservative 90; Mismatches 170; Indels 199; Gaps 20;  
 Qy 18 LPNG-INGIKDARKVTGVIGSGDFAKSLTIRLCRGVHVVGSRNPKFASEFFPHVDV 76  
 Db 60 IPKAFSGFGLEKI-----EISQNDVLEIVAN-----VFSMLPKL----- 96  
 Qy 77 THHEDALTKTNIIFVAIHREHYTSLWDLRLHLVIG-----KILIDVSN 119  
 Db 97 --HEIRIEKANNL-LYIDPDAFQNLPLNRYLLISNTGVKHLPAVHKIOSLQKVLDDIQDN 153  
 Qy 120 MRINQYPSNAYLASLPDLSLVGVFNVSNAWALQKPKDASROYVTCSSNNIARQVVI 179  
 Db 154 INIH-----TVERNFSGMISFESMILWL-----SKNGIREHNCA----- 188  
 Qy 180 ELAROLNEIPIDGLSSNARETENLPLRLFTLWRGPVVVAISLATFFFLYFVRDVIHPY 239

Db 189 -----FNGTQDELNLSDNDNLLELPNDVFNHAGSGPVILDISRTRIHSLPSYGLNKKL 243  
 Qy 240 ARNOQSDFYKPI-----EIVNKTPIVAITLL 267  
 Db 244 RARSYINLKLPTLLEKFKVTLMEASLTYSHCACAFANRRQISDLHPICNKSILRQEDVM 303  
 Qy 268 S-----LYVLAGLAAAYQLYGTKYRRP-----PPWLETWLOCRKQLG--- 306  
 Db 304 TOARGQRVSLAEDGESSLAKBFDYHVSSEFNVDLCNEVVDVICSPPKDAFNPCEDIMGDI 363  
 Qy 307 --LLSEFFAMVHVA-----YSLCLPMRSEERYFLNWAYQQVHANISWNE 351  
 Db 364 LRVLWFTSLITAITNIETLVLITVSQYKLTVP-----REFLMCLAFD----- 407  
 Qy 352 BEVWRIEYISFGIMSLGLLSLAVTISIPSVSNALNWR-----FSFTQSTLG--- 399  
 Db 408 -----LCIGIYLLIASIDIHTKSOYHNAYINWGTGACDAAGFFTFVASELSYVT 458  
 Qy 400 YVALLISTFH-----VLIYGNKRAFEERYEYRFTPPNFV-LALVLP 439  
 Db 459 LTATLWRHTTTHAMLOCKVQVRHAASIMLYGTFATFVALPFIIGISSYMKVSIQCLP 518  
 Qy 440 SIVILDLLQL 449  
 Db 519 MDIDSPLSQL 528  
 RESULT 12  
 T28379  
 ORF MSV218 hypothetical protein - Melanoplus sanguinipes entomopoxvirus  
 C:Species: Melanoplus sanguinipes entomopoxvirus  
 C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T28379  
 R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L. J. Virol. 73, 533-552, 1999  
 A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.  
 A:Reference number: Z20484; MUID:99102612  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-320 <AFO>  
 A:Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97747.1; PID:g4049787  
 C:Genetics:  
 A:Note: MSV218  
 Query Match 4.6%; Score 109; DB 2; Length 320;  
 Best Local Similarity 19.3%; Pred. No. 0.3;  
 Matches 58; Conservative 63; Mismatches 96; Indels 84; Gaps 13;  
 Qy 16 TC---LPNGINGIKDARKVTGVIGSGDFAKSLTIRLCRGVHVVGSRNPKFASEFFPH 72  
 Db 10 TCSQVINNPPLYNKDKSKVCI-----IHKNYKKILCENYHLENKSNRK---KYFDY 59  
 Qy 73 VDVTHHEDALTKTNIIFV-----AIHREHYTSLWDLRLHLVIGKILIDVSN 119  
 Db 60 ILKNIFPK--LSLESIIYNNELSKYINHIEVLYREYTKLF-----LNSNELDENHN 111  
 Qy 120 MRINQYPSNAYLASLPDLSLVKGFNVVSNAWALQKPKDASR----- 163  
 Db 112 LMVNLKSTSYSENFDFNLIKQLFNLKILDKLPKIDLPKNKHGKILFIKKNITNKKPN 171  
 Qy 164 QVYL-----CSNNIARQVIELAROLNEIPIDGLSSLSAREI---ENLPL 206  
 Db 172 NYLLYSGGIIFYNPKNNCCSNL---NNIIFKE-----ISIELASILYGGKIKYNKICN 224  
 Qy 207 RLFTLWRGPV-----VAISLATFFFLYFVRDVIHPYARNQOQSDYKPIEIVNKT 258  
 Db 225 ALYIMYKSKALKYKRYKLLKLLFPNTYDEYFKNDII---YNSNEYVDFHFNEDIYNAIKT 282  
 Qy 259 L 259  
 Db 283 L 283





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